

Notch(C)	IDEĒ-SNP	QNGGTĒ---	D-VGSY-Ē-ĒPPGFT	GK---ĒE-N
10244(C)	-NEĒTM---	QQH---Ē	VNT-ĒSY-ĒKĒ-SĒ--	G--L-Ē D
80			CRĒFPĒYT	GKT ĒSQ D
95	VNEĒGMKPRP	ĒQH R Ē	VNTĒGSYKĒFĒLS	ĒHMLP D
133	VNSRTCAMIN	ĒQYS Ē	EDTEEGPQĒĒĒPSS	ĒLRAPN
175	IDEĒASGKVI	ĒPYNRĒĒ	VNTĒGSYKĒĒHĒFE	LQYISGR
220	INEĒTMSHT	ĒSHANĒ	FNTOĒSF ĒKĒKQĒYK	ĒNGRLĒS
CR27(C)	V-ĒĒ-SG-Q--Ē-SS--Ē		-NTVĒSY-ĒKĒRĒG-W-P-PĒ-PN---	D
EGF(C)	NSDSEĒPLSHDGYĒLHDGVĒCMYIEALDKYĒĒVĒVYI---		ĒER--ĒQYRDLKWNELR	

Figure 1

[illegible]

### Figure 2

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCPGYTGKTCSQDVNECGMKPRPCQHR  
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTE  
(SEQ ID NO 3)

GWRRNSKGVCEATCEPGCKFGECVGPNNKCRCPGYTGKTCSQDVNECGMKPRPCQHR  
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAP  
NGRDCLDIDECASGKVICPYNRRCVNTFGSYCKCHIGFELQYISGRYDCIDINECTMDS  
HTCSHHANCFNTQGSFKCKCKQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAH  
KNSMKKKAKIKNVTPETRTPTPKVNLQPFNYEEIVSRGGNSHGKKGNEEKMKEGLE  
DEKREEKALKNDIEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISVDCSF  
NHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHMKDIGRLKLLLPDLQPQSN  
FCLLFDYRLAGDKVGKLRVFKNSNNALAWEKTTSEDEKWKTGKIQLYQGTDATKSIIF  
EAERGKGKTGEIADVGVLLVSGLCPSLLSVDOXMVLSLYLTLVSSLVFLILHHRTSGI  
LKLLAEKL  
(SEQ ID NO 4)

Figure 3

0981649-10501

Figure 4

ACTAGTGAATCCATCCTAATACGACTCACTATAGGGCTCGAGCGGCGCGCGGGCAGGTCTGCAGGGACAGCACCCGGTA  
ACTCCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGCGGCTTAGCTGCTACGGGGTCCGGCCGGCGCC  
CTCCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGACCCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTG  
CTCCCCCTGGGTGGCAGGTGGTTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTGTGTAGCATCGGCACGTCAGCCTGG  
GGTCTGTCACTATGGAATAAACTGGCCTGCTGCTACGGCTGGAGAAGAAAACACCAAGGGAGTCTGTCAAGCTACATGCG  
AACCTGGATGTAAGTTTGGTGAAGTGCCTGGGACCAAAACAAATGCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGT  
CAAGATGTGAATGAGTGTGGAATGAAAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGGAAGCTACAAGTGCTT  
TTGGCTCAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGGACATGTGCCATGATAAACTGTCACTATA  
CTGTGTAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGACTCCGCCTGGCCCCAAATGGAAGAGACTGT  
CTAGATATTGATGAATGTGCCTCTGGTAAAGTCATCTGTCCCTACAATCGAAGATGTGTGAACACATTGGAAGCTACTA  
CTGCAATGTACATTGGTTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACTATGG  
ATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAAGGCTCCTTCAAGTGTAAATGCAAGCAGGGATATAAA  
GGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTGTGAAGGAAGTCTCAGAGCACCTGGTACCATCAAGACAG  
AATCAAGAAAGTTGCTTGCTCAAAAAACAGCATGAAAAAGAAAGGCAAAAAATTAATAATGTTACCCCAAGAACCCACAGGA  
CTCCTACCCCTAAGGTGAACCTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACCTCATGGAGGTAAA  
AAAGGGAATGAAGAGAAAAATGAAGAGCGGGCTTGAGGATGAGAAAAGAGAAAGAGAAAGCCCTGAAGAAATGACWTAGAGGA  
GCGAAGCCTGCGAGGAGATGTGTTTTTCCCTAAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAG  
CGCTAACTTCCAACTCGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACTGGAAA  
CAGGATAGAGAAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGCTTCTATATGGCAGTTCCGGCCCTT  
GGCAGGTCAAGAAAGACATTGGCCGATTGAACTTCTCCTACCTGACCTGCAACCCCAAGCAACTTCTGTTTGCTCT  
TTGATTACCGGCTGGCCGGAGACAAAGTCCGGGAACTTCGAGTGTGTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAG  
AAGACCACGAGTGAAGGATGAAAAGTGAAGACAGGGAAATTCAGTTGTATCAAGGAAGTGTGCTACCAAAAGCATCAT  
TTTTGAAGCAGAACGTGGCCAGGGCAAAACCGGCGAAATCGCAGTGGATGGCGTCTTGCTTGTTCAGGCTTATGTCCAG  
ATAGCCTTTTATCTGTGGATGACTGAATGTTACTATCTTTATATTGACTTTGTATGTCAAGTTCCCTGGTTTTTTTGATA  
TTGSATCATAGGACCTCTGGCATTTTAAAAATTACTAAGCTGAAAAATTGTAATGTACCAACAGAAATTATTATTGTAAGA  
TGCCTTTMTTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCTTCTCAGTCATTTCTGAATCTTTC  
CACATTATATTATAAAATATGGAATGTGAGGTTTATCTCCCCCTCCTCAGTATACCTGATTGTATAAGTAAGTTGATGA  
GCTTCTCTCTGCAACATTTCTAGAAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATAGTTTTT  
TGGAAACTATGACATCAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAACTTGTATATTTAAAT  
TCTTTGTAATAATAATATCCAAATCATCAAAAAAAAAAAAAAAAAA (SEQ ID NO: 5)

Figure 5

MPLPWSLALPLLLPWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNRSKGVCEATCEPCKPFGECVGPNNKC  
RCFPGYTGKTCQSDVNECGMKPRPCQHRVCNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCOYSCEDTEEGPQCCLCP  
SGLRLAPNGRDCLDIDECASGKVICPYNARCNTFGSYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQ  
GSFKCKCKQYKGNGLRCSAIPENSVEVLRAPGTIKDRIKLLAHKNSMKKKAKIKNVTPEPTRTPTPKVNLQPFNYEE  
IVSRGGNSHGGKKGNEEKKKEGLEDEKREKALKNDXEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISV  
DCSPNHGICDWKQDREDDFDWNFPADRONAIGFYMAVPALAGHKKDIGRLKLLLPDLQPQSNFCLLPDYRLAGDKVGKLRV  
FVKNSNNALAWKTTSEDEKWKTKGIQLYQGTDAKSIIFEAERKKGKTGEIAVDGVLLVSGLCPLDLSLVDD

(SEQ ID NO: 6)

**EGFL6 (221-260 aa)  
3D Model**

**EGF  
NMR Structure**

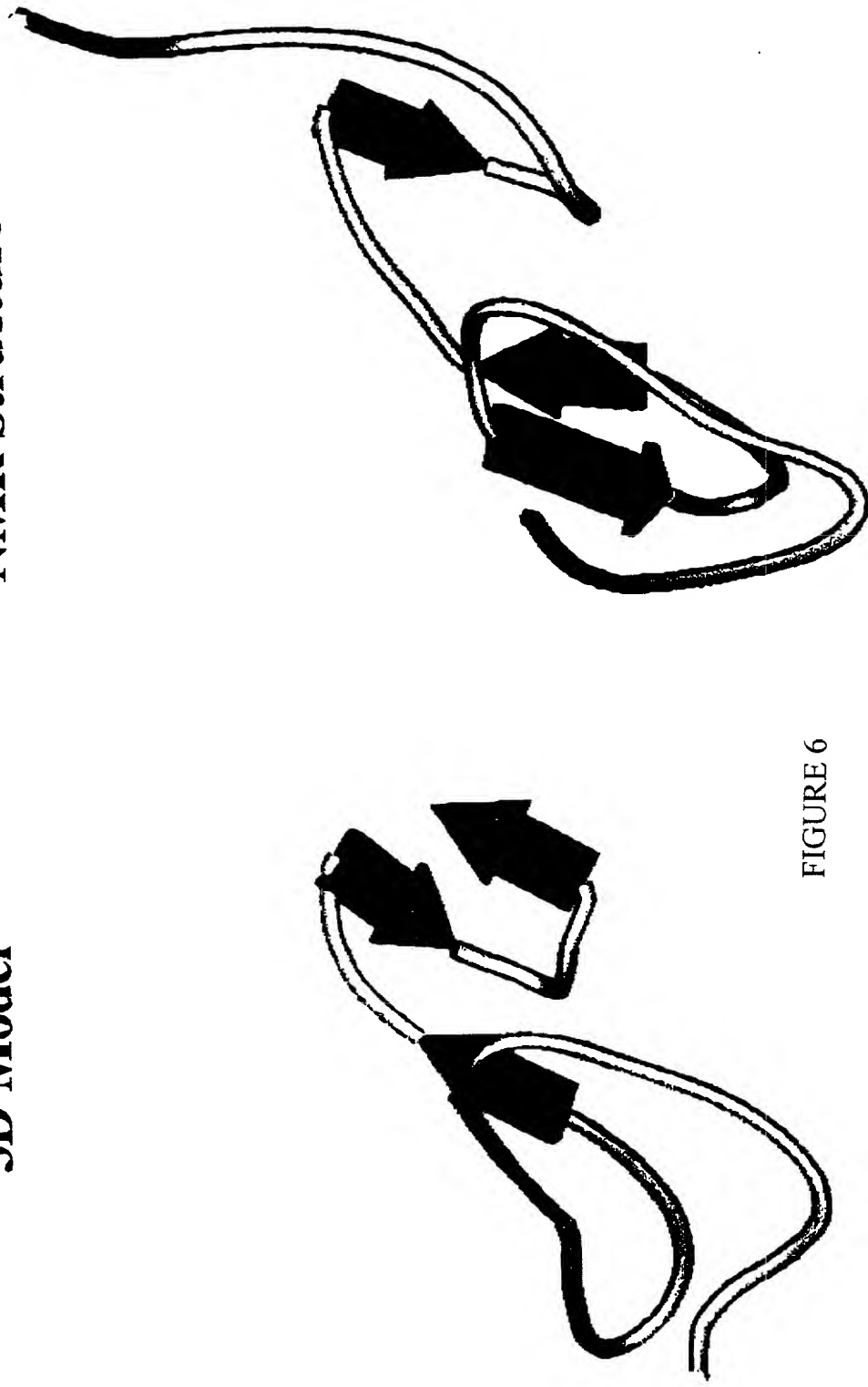


FIGURE 6